

Gencore version 4.5									
Run on:	March 1, 2001, 16:16:47	Search time	91.75	Seconds					
Title:	US-09-331-631A-5_COPY_33-75	(without alignments)							
Sequence:	1 NQEPQTEQQCORRCRQEE.....RQOYCQRCCKEICEEEBEEY	15.135	Million	cell	updates/sec				
Scoring table:	BLOSUM62								
searched:	88757 seqs., 32294092 residues								
Total number of hits satisfying chosen parameters:	88757								
Minimum DB seq length:	0								
Maximum DB seq length:	2000000000								
Post-processing:	Minimum Match 0%								
	Maximum Match 100%								
Listing first 45 summaries									
database :	Swissprot_39; *								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Length	DB ID	Description	RESULT ID	1	Scoring	Scoring	Scoring
1	105	42.3	588	1 VCLB_GOSHI	VCLB_GOSHI	STANDARD;	PRT;	588 AA.	ALIGNMENTS
2	94	37.9	605	1 VCLB_GOSHI	PO9801; CONVICILIN, CONGLICININ, ETC.	PO9801; CONVICILIN, CONGLICININ, ETC.			
3	71	28.6	47	1 AGRF_LURCY	PO9799; gossypium h	PO9799; gossypium h			
4	68	27.4	154	1 YSS1_LCAEL	PS6568; luffa cylin	PS6568; luffa cylin			
5	65.5	26.4	33	1 MBPL_MAZE	Q09662; caenorhabdi	Q09662; caenorhabdi			
6	65	26.2	919	1 ANDR_HUMAN	P28794; zea mays (m	P28794; zea mays (m			
7	64	25.8	648	1 KAPC_DICDI	P1025; homo sapien	P1025; homo sapien			
8	64	25.8	911	1 ANDR_PANTR	P24099; dictyostell	P24099; dictyostell			
9	63.5	25.6	50	1 HSPI_MOUSE	09775; pan troglod	09775; pan troglod			
10	63.5	25.6	50	1 HSPI_RAT	P02319; mus musculu	P02319; mus musculu			
11	63	25.6	626	1 AH12_ARAIV	P0118; rattus norv	P0118; rattus norv			
12	61	24.6	223	1 CAS2_SHEEP	PA3238; arachis hyp	PA3238; arachis hyp			
13	61	24.6	429	1 APA4_MACPA	P04654; ovis aries	P04654; ovis aries			
14	61	24.6	907	1 ANDR_CANPA	P33621; maccea fasc	P33621; maccea fasc			
15	60	24.2	285	1 INVO_CANPA	Q9T90; canis famili	Q9T90; canis famili			
16	59.5	24.0	614	1 AH11_ARAHY	P18174; canis famili	P18174; canis famili			
17	59	23.8	758	1 YM38_YEAST	P43237; arachis hyp	P43237; arachis hyp			
18	59	23.8	2124	1 Y192_HUMAN	Q03825; saccharomy	Q03825; saccharomy			
19	58.5	23.6	639	1 GLCX_SOBN	Q93074; homo sapien	Q93074; homo sapien			
20	58	23.6	1407	1 TRYV_RABIT	P11827; glycine max	P11827; glycine max			
21	58	23.4	223	1 CAS2_CABHI	P37709; oryctolagus	P37709; oryctolagus			
22	58	23.4	644	1 BTD_DROME	P33049; capra hircu	P33049; capra hircu			
23	58	23.4	2318	1 NTG3_MOUSE	024266; drosophila	024266; drosophila			
24	57.5	23.2	338	1 FSA_HUMAN	Q93072; mus musculu	Q93072; mus musculu			
25	57.5	23.2	605	1 GLCA_SOBN	P19883; homo sapien	P19883; homo sapien			
26	57	23.0	991	1 DHP1_SCIPPO	P13916; glycine max	P13916; glycine max			
27	57	23.0	210	1 YQER_ECOLI	P40948; schizosacch	P40948; schizosacch			
28	57	23.0	1898	1 TRYV_HUMAN	Q46941; escherichia	Q46941; escherichia			
29	57	23.0	1905	1 TAGB_DICDI	Q07283; homo sapien	Q07283; homo sapien			
30	56.5	22.8	284	1 TPM1_RAT	P54663; dictyosteli	P54663; dictyosteli			
31	56.5	22.8	284	1 TPM2_HUMAN	P06395; rattus norv	P06395; rattus norv			
32	55.5	22.8	284	1 TPM3_HUMAN	P06468; homo sapien	P06468; homo sapien			
33	56.5	22.8	284	1 TPMB_RABBIT	P07951; homo sapien	P07951; homo sapien			
					P02560; orctolagus	P02560; orctolagus			

DT 01-OCT-1996 (Rel. 34. Last annotation update)

DE ANTIMICROBIAL PEPTIDE MFP-1.

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

RN [1]

RP SQUOENCE.

RC STRAIN=CV; B73; TISSUE=SEED;

RC MEDLINE=92406801; PubMed=1527010;

RA Divick J.P., Rood T., Rao A.G., Marshak D.R.;

RT "Purification and characterization of a novel antimicrobial peptide

RT from maize (zea mays L.) kernels.";

RL J. Biol. Chem. 267:18814-18820(1992).

CC C - FUNCTION: INHIBITOR OF BOTH BACTERIAL AND FUNGAL GROWTH IN VITRO.

CC - TISSUE SPECIFICITY: PREDOMINANTLY IN THE EMBRYO PORTION OF THE

CC KERNEL.

DR PIR; AA1822; A41822.

DR M12ZDB; 69182;

KW Fungicide; Antibiotic.

SEQUENCE 33 AA; 4131 MW; B148F1B90E823599 CRC64;

Query Match 26.4%; Score 65.5; DB 1; Length 33;

Best Local Similarity 44.0%; Pred. No. 0.49; PRT; 919 AA.

Matches 11; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Oy 11 OCORRC-RQESDPROOYCORRCK 34

Db 6 ECRRQCLRRHEGQPWETQECMRRCR 30

RESULT 6

ANDR_HUMAN STANDARD; PRT; 919 AA.

ID P10275; 01-MAR-1989 (rel. 10, Created)

AC DT 01-APR-1990 (rel. 14, Last sequence update)

DE DT 01-OCT-2000 (rel. 40, Last annotation update)

DE ANDROGEN RECEPTOR (DHYDROESTROSTEROINE RECEPTOR).

GN AR OR NR3C4 OR DHTR.

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo.

RN [1]

RP SEQUENCE FROM N_A.

RX MEDLINE=89112208; PubMed=3216866;

RA Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E.,

RA French F.S., Wilson E.M.;

RT "The human androgen receptor: complementary deoxyribonucleic acid

RT cloning, sequence analysis and gene expression in prostate.";

RL Mol. Endocrinol. 2:1265-1275(1998).

RN [2]

RP SEQUENCE FROM N_A.

RX MEDLINE=90083302; PubMed=2594783;

RA Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Miseon C.J.,

RA Wilson E.M., French F.S.;

RT "Sequence of the intron/exon junctions of the coding region of the

RT human androgen receptor gene and identification of a point mutation

RT in a family with complete androgen insensitivity.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:9534-9538(1989).

RN [3]

RP SEQUENCE FROM N_A.

RX MEDLINE=90258935; PubMed=2342476;

RA Govinden M.V.;

RC TISSUE=PROSTATE;

RC MEDLINE=89017168; PubMed=3174628;

RA "Specific region in hormone binding domain is essential for hormone

RT binding and trans-activation by human androgen receptor.";

RL Mol. Endocrinol. 4:417-427(1990).

RN [4]

RP SEQUENCE FROM N_A.

RA "Structural analysis of complementary DNA and amino acid sequences of

RT

RT human and rat androgen receptors.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215(1988).

RN [5]

RP SQUENCE FROM N_A.

RT TISSUE=PROSTATE;

RC MEDLINE=89028909; PubMed=2011578;

RA Tilley W.D., Marcelli M., Wilson J.D., McPhaul M.J.;

RT "Characterization and expression of a cDNA encoding the human androgen receptor.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:327-331(1989).

RN [6]

RP SQUENCE FROM N_A.

RC TISSUE=PROSTATE;

RC MEDLINE=91155943; PubMed=2293020;

RA Marcelli M., Tilley W.D., Wilson C.M., Griffin J.E., Wilson J.D.,

RA McPhaul M.J.;

RT "Definition of the human androgen receptor gene structure permits the identification of mutations that cause androgen resistance: premature termination of the receptor protein at amino acid residue 588 causes complete androgen resistance.";

RT Mol. Endocrinol. 4:1105-1116(1990).

RN [7]

RP SQUENCE OF 189-919 FROM N_A.

RX MEDLINE=8817811; PubMed=335376;

RA Chang C., Kokontis J., Liao S.;

RT "Molecular cloning of human and rat complementary DNA encoding androgen receptors.";

RL Science 240:324-326(1988).

RN [8]

RP SQUENCE OF 468-919 FROM N_A.

RX MEDLINE=88240407; PubMed=3377788;

RA Trapman J., Klaassen P., Kuiper G.G.J.M., van der Korput J.A.G.M.,

RA Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voorhorst M.M.,

RA Mulder E., Brinkmann A.O.;

RT "Cloning, structure and expression of a cDNA encoding the human androgen receptor.";

DT androgen receptor.";

RL Blochem. Biophys. Res. Commun. 153:241-248(1988).

RN [9]

RP POLYMORPHISM OF POLY-GLN REGION

RX MEDLINE=92220629; PubMed=1561105;

RA Stedden H.F., Oostra B.A., Brinkmann A.O., Trapman J.;

RT "Trinucleotide repeat polymorphism in the androgen receptor gene (AR)." ;

RL Nucleic Acids Res. 20:1427-1427(1992).

RN [10]

RP POLYMORPHISM OF POLY-GLY REGION

RC TISSUE=BLOOD;

RA Lu J., Danielsen M.;

RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

RN [11]

RL VARIANTS S9MA IN POLY-GLN REGION

RX MEDLINE=91287825; PubMed=2062300;

RA Spada A.R., Wilson E.M., Lubahn D.B., Harding A.E., Fischbeck K.H.;

RT "Androgen receptor gene mutations in X-linked spinal and bulbar muscular atrophy";

RT Nature 352:77-79(1991).

RN [12]

RP REVIEW ON VARIANTS.

RX MEDLINE=91223089; PubMed=7937037;

RA Patterson M.N., Hughes L.A., Gottlieb B., Pinsky L.;

RT "Androgen receptor gene mutations in databases.";

RL Nucleic Acids Res. 22:3560-3562(1994).

RN [13]

RP REVIEW ON VARIANTS.

RX MEDLINE=97169385; PubMed=9016538;

RA Gottlieb B., Trifiro M., Lubrano R., Vassilou D.M., Pinsky L.;

RT "The androgen receptor gene mutations database.";

RL Nucleic Acids Res. 25:158-162(1997).

RN [14]

RP VARIANT LNCAP ALA-877.

RX MEDLINE=91083633; PubMed=2260966;

RA Welscholte J., Ris-Stalpers C., Kuiper G.G., Jenster G.,

RA Berrevoets C., Claassen E., van Rooij H.C.J., Trapman J.,

RA

RA Brinkmann A.O., Mulder E.;
RT "A mutation in the ligand binding domain of the androgen receptor of
human LNCaP cells affects steroid binding characteristics and
response to anti-androgens.";
RL Biochem. Biophys. Res. Commun. 173:534-540(1990).
[15]

RP VARIANT CA153 M29>R665;
RX MEDLINE=9116693; PubMed=2082179;
RA Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J.,
RA Corfen J.L.;
RT "Functional characterization of naturally occurring mutant androgen
receptors from subjects with complete androgen insensitivity.";
RL Mol. Endocrinol. 4:1759-1772(1990).
RN [16]

RP VARIANT CYS>74;
RX MEDLINE=91310758; PubMed=1856263;
RA Marcelli M., Tilley W.D., Zorppi S., Griffin J.E., Wilson J.D.,
RA McPhaul M.J.;
RT "Androgen resistance associated with a mutation of the androgen
receptor at amino acid 72 (Arg-->Cys) results from a combination of
decreased messenger ribonucleic acid levels and impairment of
receptor function.";
RL J. Clin. Endocrinol. Metab. 73:318-325(1991).
RN [17]

RP VARIANT CA153 ASN-695 AND HIS-695, AND SEQUENCE OF 629-723 FROM N.A.
RX MEDLINE=91751307; PubMed=1775137;
RA Ris-Stalpers C., Trikro M.A., Kuiper G.G., Jenster G., Romalo G.,
RA Sai T., van Rooijen C., Kaufman M., Rosenfeld R.L., Liao S.;
RT "Substitution of aspartic acid-686 by histidine or asparagine in the
human androgen receptor leads to a functionally inactive protein with
altered hormone-binding characteristics.";
RL Mol. Endocrinol. 5:1562-1569(1991).
RN [18]

RP VARIANT CA153 AND P450.
RX MEDLINE=91338440; PubMed=1307250;
RA Batch J.A., Williams D.M., Davies H.R., Brown B.D., Evans B.A.J.,
RA Hughes T.A., Patterson M.N.;
RT "Androgen receptor gene mutations identified by SSCP in fourteen
subjects with androgen insensitivity syndrome.";
RL Hum. Mol. Genet. 1:497-503(1992).
RN [19]

RP VARIANT CA153 VAL-787.
RX MEDLINE=92235226; PubMed=1569163;
RA Nakao R., Haji M., Yanase T., Ogo A., Takayanagi R., Katsube T.,
RA Fukunaki Y., Nawata H.;
RT "A single amino acid substitution (Met-786-->Val) in the steroid-
binding domain of human androgen receptor leads to complete androgen
insensitivity syndrome.";
RL J. Clin. Endocrinol. Metab. 74:1152-1157(1992).
RN [20]

RP VARIANT LNCAP ALA-877.
RX MEDLINE=9222955; PubMed=1562539;
RC Veldschoot J., Berrevoets C.A., Ris-Stalpers C., Kuiper G.G.,
RA Jenster G., Trapman J., Brinkmann A.O., Mulder E.,
RT "The androgen receptor in LNCaP cells contains a mutation in the
ligand binding domain which affects steroid binding characteristics
and response to anti-androgens.";
RL J. Steroid Biochem. Mol. Biol. 41:665-669(1992).
RN [21]

RP VARIANT MET>730.
RX MEDLINE=92335289; PubMed=1631125;
RA Newmark J.R., Hardy D.O., Tomb D.C., Carter B.S., Epstein J.L.,
RA Isaacs W.B., Brown T.R., Barrack E.R.;
RT "Androgen receptor gene mutations in human prostate cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6319-6323(1992).
RN [22]

RP VARIANT CA153 VAL-754.
RX MEDLINE=93372806; PubMed=8103398;
RA Lobaccaro J.-M., Lumbruso S., Ktari R., Dumas R., Sultan C.;
RT "An exotic point mutation creates a MaeII site in the androgen
receptor gene of a family with complete androgen insensitivity
syndrome.";
RL Hum. Mol. Genet. 2:1041-1043(1993).

RP VARIANT CA153 ARG-807.
RX MEDLINE=94108430; PubMed=8281140;
RA Adeyemo O., Kallio P.J., Palvimo J.J., Kontula K., Jaenne O.A.;
RT "A single-base substitution in exon 6 of the androgen receptor gene
causing complete androgen insensitivity: the mutated receptor fails
to transactivate but binds to DNA in vitro.";
RL Hum. Mol. Genet. 2:1809-1812(1993).
RN [24]

RP VARIANT P450 VAL>743.
RX MEDLINE=9315568; PubMed=8325932;
RA Nakao R., Yanase T., Sasaki Y., Haji M., Nawata H.;
RT "A single amino acid substitution (Gly743 --> Val) in the steroid-
binding domain of the human androgen receptor leads to Reifenstein
syndrome.";
RN [25]

Query Match 26.2%; Score 65; DB 1; Length 919;
Best Local Similarity 48.3%; Pred. No. 8.2;
Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
Db 61 QQQQQQQQQQQQQQQQQERTSPQQQQQ 89

RESULT 7
KAPC_DICDI ID KAPC_DICDI STANDARD PRT; 648 AA.
AC P34059;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (EC 2.7.1.37).
GN PKAC OR PK2 OR PK3.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyosteliida; Dictyostelium.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=91323730; PubMed=1864510;
RA Buerki E., Anjard C., Scholde J.-C., Raymond C.D.;
RT "Isolation of two genes encoding putative protein kinases regulated
during Dictyostelium discoideum development.";
RL Gene 102:57-65(1991).
RN [2]

RP CHARACTERIZATION.
RX MEDLINE=93385090; PubMed=8373760;
RA Anjard C., Etchebehere L., Pinaud S., Veron M., Raymond C.D.;
RT "An unusual catalytic subunit for the cAMP-dependent protein kinase
of Dictyostelium discoideum.";
RL Biochemistry 32:9532-9538(1993).
RN [3]

RP CHARACTERIZATION.
RX MEDLINE=93066311; PubMed=1332055;
RA Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.;
RT "Dapk3, which plays essential roles during Dictyostelium development,
encodes the catalytic subunit of cAMP-dependent protein kinase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).
CC -1- FUNCTION: ESSENTIAL FOR DIFFERENTIATION AND FRUIT MORPHOGENESIS.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
CC -1- SUBUNIT: IN DICTYOSTELIUM THE HOLOENZYME IS A DIMER COMPOSED OF
A REGULATORY (R) AND A CATALYTIC (C) SUBUNIT. IN THE PRESENCE OF
CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER.
CC -1- DEVELOPMENTAL STAGE: CAPK ACTIVITY IS LOW IN VEGETATIVELY GROWING
CC AMOEBAE, INCREASES DURING DEVELOPMENT OF AGGREGATION AND REACHES
CC A MAXIMUM AT COMPLICATION.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMP SUBFAMILY.

CC -----
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DR EMBL; M38703; -; NOT_ANNOTATED_CDS.

DR PIR; JQ1150; JQ1150.

DR HSSP; P05132; 2CPR.

DR DICTYDB; DD02030; PKAC.

DR INTERPRO; IPR00719; -.

DR INTERPRO; IPR000561; -.

DR INTERPRO; IPR002290; -.

DR PFAM; PFO0059; kinase; 1.

DR PFAM; PFO0433; phosphatase; C; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding; cAMP;

KW phosphorylation.

FT DOMAIN_58 64 ASN-RICH.

FT DOMAIN 136 223 GLN-RICH.

FT DOMAIN 233 250 THR-RICH.

FT DOMAIN 336 590 PROTEIN KINASE.

FT NP_BIND 342 350 ATP (BY SIMILARITY).

FT BINDING 365 365 ATP (BY SIMILARITY).

FT ACT_SITE 459 459 BY SIMILARITY.

FT MOD_RES 490 490 PHOSPHORYLATION (BY SIMILARITY).

FT SEQUENCE 648 AA; 74458 MW; D0F9B3A48C58D084 CRC64;

SQ

Query Match 25.8%; Score 64; DB 1; Length 648;

Best Local Similarity 29.3%; Pred. No. 7; Mismatches 12; Conservative 15; Indels 0; Gaps 0; Matches 12; Mismatches 14; Gaps 0;

QY 2 QEDPQTEQQCQCORRCRQESDPRRQQVQCRKKEICEEEEE 42

Db 145 QQQPQQQQPQQQQPQQQQQQQQQQQQQQQQQQQQQQQQ 185

RESULT 8

ANDR_PANTR ID STANDARD; PRT; 911 AA.

AC 09775;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).

GN AR OR NR3C4.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98404153; PubMed=9732460;

RA Choong C.S., Kempainen J.A., Wilson E.M.;

RT Evolution of the primate androgen receptor: a structural basis for disease. ";

RL J. Mol. Evol. 47:334-342(1998).

-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

CC NR3 SUBFAMILY.

CC

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CC

DR EMBL; U94177; AAC73048.1; -.

DR IISPP; P06536; 1RCD.

DR INTERPRO; IPR00536; -.

DR INTERPRO; IPR001103; -.

DR INTERPRO; IPR001628; -.

DR PFAM; PFO0104; hormone_rec; 1.

DR PFAM; PFO0105; ZF-C4; 1.

DR PRINTS; PR00047; STROIDFINGER.

DR PROSITE; PS00031; NUCLEAR_RECEPATOR; 1.

KW receptor; Transcription regulation; DNA-binding; nuclear protein; Zinc-finger; Steroid-binding.

FT DOMAIN 1 549 MODULATING (BY SIMILARITY).

FT DNA_BIND 551 C4-TYPE ZINC FINGERS (TWO).

FT ZN_FING 551 C4-TYPE.

FT DOMAIN 587 611 C4-TYPE.

FT DOMAIN 682 911 LIGAND-BINDING.

FT DOMAIN 57 78 POLY-GN.

FT DOMAIN 84 88 POLY-GN.

FT DOMAIN 192 196 POLY-GN.

FT DOMAIN 371 380 POLY-PRO.

FT DOMAIN 395 401 POLY-ALA.

FT DOMAIN 448 454 POLY-GX.

SQ SEQUENCE 911 AA; 98402 MW; 601BB4D4E697DAA4 CRC64;

Query Match 25.8%; Score 64; DB 1; Length 911;

Best Local Similarity 50.0%; Pred. No. 10; Mismatches 6; Indels 0; Gaps 0; Matches 13; Conservative 6; Mismatches 7; Gaps 0;

QY 2 QEDPQTEQQCQCORRCRQESDPRRQQVQCRKKEICEEEEE 27

Db 61 000QQQQQQQQQQQQQQQQQQQQQQETSPRQQQ 86

RESULT 9

HSPL_MOUSE ID HSPL_MOUSE STANDARD; PRT; 50 AA.

AC P02319;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).

DR PRM1 OR PRM-1.

OS Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8519903; PubMed=2986684;

RA Kleene K.C., Distel R.J., Hecht N.B.;

RT "Nucleotide sequence of a cDNA clone encoding mouse protamine 1.";

RL Biochemistry 24:719-722(1985).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=88193065; PubMed=3358932;

RA Johnson P.A., Pschon J.J., Yellick P.C., Palmiter R.D., Hecht N.B.;

RT "Sequence homologies in the mouse protamine 1 and 2 genes.";

RL Biochim. Biophys. Acta 950:45-53(1988).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=87260978; PubMed=3037541;

RA Peschon J.J., Behringer R.R., Brinster R.L., Palmiter R.D.;

RT "Spermatid-specific expression of protamine 1 in transgenic mice.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:5316-5319(1987).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=88181903; PubMed=3445973;

RA Hecht N.B.;

RT "Gene expression during spermatogenesis.";

RL Ann. N.Y. Acad. Sci. 513:90-101(1987).

RN [5]

SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.
 RC STRAIN=CV FLORUNNER;
 RX MEDLINE=96013631; PubMed=7560062;
 RA Burks A.W., Cockrell I.G., Stanley J.S., Helm R.M., 'Bannon G.A.';
 RT "Recombinant peanut allergen Ara h 1 expression and IgE binding in patients with peanut hypersensitivity.";
 RL J. Clin. Invest. 96:1715-1721(1995).
 CC -!- SIMILARITY: TO 75 SEED STORAGE PROTEINS (PHASEOLIN, VICTILIN, CONVICILIN, CONGLICININ, ETC.).
 CC -----
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 CC -----
 CC EMBL; L34402; AABU0861.1; -.
 DR HSSP; P50477; 1CAW
 DR INTERPRO; IPR001113; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 KW Allergen.
 SQ SEQUENCE 626 AA: 71345 MW: 1N6BBBE41490D0E3 CRC64;
 RESULT 12
 CAS2_SHBEP STANDARD; PRT; 223 AA.
 ID CAS2_SHBEP STANDARD; PRT; 223 AA.
 AC P04654;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ALPHA-S2 CASEIN PRECURSOR.
 GN CEN1S2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86104467; PubMed=3002499;
 RA Boinbard M., Petrisant G.;
 RT "Complete sequence of ovine alpha s2-casein messenger RNA.";
 RL Blochini 67:1043-1051(1985).
 CC -!- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT CALCIUM PHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
 CC -!- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; X03238; CAA26983.1; -.
 DR PIR; A25070; KASH2.
 DR INTERPRO; IPR001588; -.
 DR PFAM; PF00363; caseins; 2.
 DR PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
 KW Milk: Phosphorylation: Signal.
 FT SIGNAL=15
 FT CHAIN 16 223 ALPHA-S2 CASEIN.
 FT REPEAT 77 141
 FT REPEAT 159 223
 FT MOD_RES 23 23
 FT MOD_RES 24 24 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 25 25 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 72 72 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 73 73 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 74 74 PHOSPHORYLATION (POTENTIAL).
 FT VARIANT 64 64 D -> N.
 SQ SEQUENCE 223 AA: 26332 MW: 67212935E27426D7 CRC64;
 RESULT 13
 ID APA4_MACFA STANDARD; PRT; 429 AA.
 AC P33621;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV).
 GN APOA4.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopithecinae; Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=LEUKOCYTE;
 RA MEDLINE=93192330; PubMed=9448212;
 RA Osada J., Rocovi M., Nicodosi R.J., Schaefer E.J., Ordovas J.M.;
 RT "Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III and A-IV genes.",
 RL Biochim. Biophys. Acta 1172:335-339(1993).
 CC -!- FUNCTION: MAY HAVE A ROLE IN CHYLOMORONS AND VLDL SECRETION AND CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR COMPONENT OF HDL AND CHYLOMORONS.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: SECRETED IN PLASMA.
 CC -!- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (FACH 22-MER) IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOE FAMILY.
 CC -----
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 CC -----
 CC EMBL; X68361; CAA48421.1; -.
 DR PIR; S29565; S29565.
 DR PIR; S30195; S30195.
 DR HSSP; P02649; INFO.
 DR INTERPRO; IPR000074; -.
 DR PFAM; PF01442; Apolipoprotein; 1.

KW	Plasma: Lipid transport; HDL: Chylomicron; Repeat; Signal.
FT	SIGNAL 1 20
FT	CHAIN 21 429
FT	DOMAIN 33 330
FT	REPEAT 33 54
FT	REPEAT 60 81
FT	REPEAT 82 103
FT	REPEAT 115 136
FT	REPEAT 137 158
FT	REPEAT 159 180
FT	REPEAT 181 202
FT	REPEAT 203 224
FT	REPEAT 225 246
FT	REPEAT 247 268
FT	REPEAT 269 286
FT	REPEAT 287 308
FT	REPEAT 309 330
FT	DOMAIN 372 420
SQ	SEQUENCE 429 AA; 49876 MW; 3D458F551D0DB60C CRC64;
RESULT 14	
ANDR_CANFA	STANDARD; PRT; 907 AA.
AC	Q91P0;
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DT	DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RBCEPIOR).
GN	AR OR NR3C4.
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ocellata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MIDLINE=90348475; PubMed=2385171;
RA	Tseng, H., Green, H.,
RT	"The involucrin genes of pig and dog: comparison of their segments of repeats with those of prosimians and higher primates.";
RL	Mol. Biol. Evol. 7: 293-302 (1990).
CC	-1- FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO MEMBRANE PROTEINS BY TRANSLUTAMINASE. ALL THAT RESULTS IN THE FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.
CC	-1- TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND OTHER STRATIFIED SQUAMOUS EPITHELIUM.
CC	-----
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CC	-----
CC	DR EMBL; M34412; AAA30853.1; -.
CC	DR INVERPRO; IPR0023360; -.
CC	DR PROSITE; PS00795; INVOLUCRIN; 1.
CC	SEQUENCE 285 AA; 33384 MW; DCE1BD88B9248BEA CRC64;
DR	EMBL; AF197950; AAF18084.1; -.
DR	PROSTIE; PS00321; NUCLEAR RECEPTOR; 1.
CC	Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
CC	DOMAIN 1 545 MODULATING (BY SIMILARITY).
FT	DNA_BIND 547 612 C4-TYPE ZINC FINGERS (TWO).
FT	ZN_FING 547 567 C4-TYPE.
FT	ZN_FING 583 607 C4-TYPE.
RESULT 15	
INVO_CANFA	STANDARD; PRT; 285 AA.
TD	INVO_CANFA
AC	P18174;
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	01-FEB-1995 (Rel. 33, Last annotation update)
DE	INVOLUCRIN.
GN	IVL.
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ocellata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MIDLINE=90348475; PubMed=2385171;
RA	Tseng, H., Green, H.,
RT	"The involucrin genes of pig and dog: comparison of their segments of repeats with those of prosimians and higher primates.";
RL	Mol. Biol. Evol. 7: 293-302 (1990).
CC	-1- FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO MEMBRANE PROTEINS BY TRANSLUTAMINASE. ALL THAT RESULTS IN THE FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.
CC	-1- TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND OTHER STRATIFIED SQUAMOUS EPITHELIUM.
CC	-----
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CC	-----
CC	DR EMBL; M34412; AAA30853.1; -.
CC	DR INVERPRO; IPR0023360; -.
CC	DR PROSITE; PS00795; INVOLUCRIN; 1.
CC	SEQUENCE 285 AA; 33384 MW; DCE1BD88B9248BEA CRC64;
DR	EMBL; AF197950; AAF18084.1; -.
DR	PROSTIE; PS00321; NUCLEAR RECEPTOR; 1.
CC	Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
CC	DOMAIN 1 545 MODULATING (BY SIMILARITY).
FT	DNA_BIND 547 612 C4-TYPE ZINC FINGERS (TWO).
FT	ZN_FING 547 567 C4-TYPE.
FT	ZN_FING 583 607 C4-TYPE.
Query Match	24.6%; Score 61; DB 1; Length 285;
Best Local Similarity	34.1%; Pred. No. 10;
Matches	13; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
OY	2 QEDPOTECQCQCORRCQEQESPRQQYCQQRCKECEEEEEE 42
Db	142 QQQEQQEQQEKEBLHLQEQQREELQQEQQQGKEQCKHQE 182

